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SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT:
 (A) NAME: Forschungszentrum Borstel
 (B) STREET: Parkallee 1-40
 (C) CITY: Borstel
 (D) State: Schleswig-Holstein
 (E) COUNTRY: Germany
 (F) POSTAL CODE: D 23845
- (ii) TITLE OF INVENTION: Antisense-Oligonucleotides for treating proliferating cells
- (iii) NUMBER OF SEQUENCES: 3
- (iv) COMPUTER READABLE FORM:
 (A) MEDIUM TYPE: Floppy disk
 (B) COMPUTER: IBM PC compatible
 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPA)

(2) INFORMATION FOR SEQ ID NO: 1:

- (i) SEQUENZ CHARACTERISTICS:
 (A) LENGTH: 12493 base pairs
 (B) TYPE: Nucleotid
 (C) STRANDEDNESS: double strand
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNS
- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 197..9964

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

45	CTACCGGGCG GAGGTGAGCG CGGCGCCGGC TCCTCCTGCG GCGGACTTTG	60
	GACGAGCGGT GGTCGACAA GTGGCCTTGC GGGCCGGATC GTCCCAGTGG AAGAGTTGTA	120
	AATTTGCTTC TGGCCTTCCC CTACGGATTA TACCTGGCCT TCCCCTACGG ATTATACTCA	180
50	ACTTACTGTT TAGAAA ATG TGG CCC ACG AGA CGC CTG GTT ACT ATC AAA	229
	Met Trp Pro Thr Arg Arg Leu Val Thr Ile Lys	
	1 5 10	
55	AGG AGC GGG GTC GAC GGT CCC CAC TTT CCC CTG AGC CTC AGC ACC TGC	277
	Arg Ser Gly Val Asp Gly Pro His Phe Pro Leu Ser Leu Ser Thr Cys	
	15 20 25	
60	TTG TTT GGA AGG GGT ATT GAA TGT GAC ATC CGT ATC CAG CTT CCT GTT	325
	Leu Phe Gly Arg Gly Ile Glu Cys Asp Ile Arg Ile Gln Leu Pro Val	
	30 35 40	
65	GTG TCA AAA CAA CAT TGC AAA GTT GAA ATC CAT GAG CAG GAG GCA ATA	373
	Val Ser Lys Gln His Cys Lys Val Glu Ile His Glu Gln Glu Ala Ile	
	45 50 55	

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	TTA CAT AAT TTC AGT TCC ACA AAT CCA ACA CAA GTA AAT GGG TCT GTT	421
	Leu His Asn Phe Ser Ser Thr Asn Pro Thr Gln Val Asn Gly Ser Val	
	60 65 70 75	
5	ATT GAT GAG CCT GTA CGG CTA AAA CAT GGA GAT GTA ATA ACT ATT ATT	469
	Ile Asp Glu Pro Val Arg Leu Lys His Gly Asp Val Ile Thr Ile Ile	
	80 85 90	
10	GAT CGT TCC TTC AGG TAT GAA AAT GAA AGT CTT CAG AAT GGA AGG AAG	517
	Asp Arg Ser Phe Arg Tyr Glu Asn Glu Ser Leu Gln Asn Gly Arg Lys	
	95 100 105	
15	TCA ACT GAA TTT CCA AGA AAA ATA CGT GAA CAG GAG CCA GCA CGT CGT	565
	Ser Thr Glu Phe Pro Arg Lys Ile Arg Glu Gln Glu Pro Ala Arg Arg	
	110 115 120	
20	GTC TCA AGA TCT AGC TTC TCT GAC CCT GAT GAG AAA GCT CAA GAT	613
	Val Ser Arg Ser Ser Phe Ser Ser Asp Pro Asp Glu Lys Ala Gln Asp	
	125 130 135	
25	TCC AAG GCC TAT TCA AAA ATC ACT GAA GGA AAA GTT TCA GGA AAT CCT	661
	Ser Lys Ala Tyr Ser Lys Ile Thr Glu Gly Lys Val Ser Gly Asn Pro	
	140 145 150 155	
30	CAG GTA CAT ATC AAG AAT GTC AAA GAA GAC AGT ACC GCA GAT GAC TCA	709
	Gln Val His Ile Lys Asn Val Lys Glu Asp Ser Thr Ala Asp Asp Ser	
	160 165 170	
35	AAA GAC AGT GTT GCT CAG GGA ACA ACT AAT GTT CAT TCC TCA GAA CAT	757
	Lys Asp Ser Val Ala Gln Gly Thr Thr Asn Val His Ser Ser Glu His	
	175 180 185	
40	GCT GGA CGT AAT GGC AGA AAT GCA GCT GAT CCC ATT TCT GGG GAT TTT	805
	Ala Gly Arg Asn Gly Arg Asn Ala Ala Asp Pro Ile Ser Gly Asp Phe	
	190 195 200	
45	AAA GAA ATT TCC AGC GTT AAA TTA GTG AGC CGT TAT GGA GAA TTG AAG	853
	Lys Glu Ile Ser Ser Val Lys Leu Val Ser Arg Tyr Gly Glu Leu Lys	
	205 210 215	
50	TCT GTT CCC ACT ACA CAA TGT CTT GAC AAT AGC AAA AAA AAT GAA TCT	901
	Ser Val Pro Thr Thr Gln Cys Leu Asp Asn Ser Lys Lys Asn Glu Ser	
	220 225 230 235	
55	CCC TTT TGG AAG CTT TAT GAG TCA GTG AAG AAA GAG TTG GAT GTA AAA	949
	Pro Phe Trp Lys Leu Tyr Glu Ser Val Lys Lys Glu Leu Asp Val Lys	
	240 245 250	
60	TCA CAA AAA GAA AAT GTC CTA CAG TAT TGT AGA AAA TCT GGA TTA CAA	997
	Ser Gln Lys Glu Asn Val Leu Gln Tyr Cys Arg Lys Ser Gly Leu Gln	
	255 260 265	
65	ACT GAT TAC GCA ACA GAG AAA GAA AGT GCT GAT GGT TTA CAG GGG GAG	1045
	Thr Asp Tyr Ala Thr Glu Lys Glu Ser Ala Asp Gly Leu Gln Gly Glu	
	270 275 280	
70	ACC CAA CTG TTG GTC TCG CGT AAG TCA AGA CCA AAA TCT GGT GGG AGC	1093
	Thr Gln Leu Leu Val Ser Arg Lys Ser Arg Pro Lys Ser Gly Gly Ser	
	285 290 295	
75	GGC CAC GCT GTG GCA GAG CCT GCT TCA CCT GAA CAA GAG CTT GAC CAG	1141
	Gly His Ala Val Ala Glu Pro Ala Ser Pro Glu Gln Glu Leu Asp Gln	
	300 305 310 315	

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	AAC AAG GGG AAG GGA AGA GAC GTG GAG TCT GTT CAG ACT CCC AGC AAG Asn Lys Gly Lys Gly Arg Asp Val Glu Ser Val Gln Thr Pro Ser Lys 320 325 330	1189
5	GCT GTG GGC GCC AGC TTT CCT CTC TAT GAG CCG GCT AAA ATG AAG ACC Ala Val Gly Ala Ser Phe Pro Leu Tyr Glu Pro Ala Lys Met Lys Thr 335 340 345	1237
10	CCT GTA CAA TAT TCA CAG CAA CAA AAT TCT CCA CAA AAA CAT AAG AAC Pro Val Gln Tyr Ser Gln Gln Gln Asn Ser Pro Gln Lys His Lys Asn 350 355 360	1285
15	AAA GAC CTG TAT ACT ACT GGT AGA AGA GAA TCT GTG AAT CTG GGT AAA Lys Asp Leu Tyr Thr Thr Gly Arg Arg Glu Ser Val Asn Leu Gly Lys 365 370 375	1333
20	AGT GAA GGC TTC AAG GCT GGT GAT AAA ACT CTT ACT CCC AGG AAG CTT Ser Glu Gly Phe Lys Ala Gly Asp Lys Thr Leu Thr Pro Arg Lys Leu 380 385 390 395	1381
25	TCA ACT AGA AAT CGA ACA CCA GCT AAA GTT GAA GAT GCA GCT GAC TCT Ser Thr Arg Asn Arg Thr Pro Ala Lys Val Glu Asp Ala Ala Asp Ser 400 405 410	1429
30	GCC ACT AAG CCA GAA AAT CTC TCT TCC AAA ACC AGA GGA AGT ATT CCT Ala Thr Lys Pro Glu Asn Leu Ser Ser Lys Thr Arg Gly Ser Ile Pro 415 420 425	1477
35	ACA GAT GTG GAA GTT CTG CCT ACG GAA ACT GAA ATT CAC AAT GAG CCA Thr Asp Val Glu Val Leu Pro Thr Glu Thr Glu Ile His Asn Glu Pro 430 435 440	1525
40	TTT TTA ACT CTG TGG CTC ACT CAA GTT GAG AGG AAG ATC CAA AAG GAT Phe Leu Thr Leu Trp Leu Thr Gln Val Glu Arg Lys Ile Gln Lys Asp 445 450 455	1573
45	TCC CTC AGC AAG CCT GAG AAA TTG GGC ACT ACA GCT GGA CAG ATG TGC Ser Leu Ser Lys Pro Glu Lys Leu Gly Thr Thr Ala Gly Gln Met Cys 460 465 470 475	1621
50	TCT GGG TTA CCT GGT CTT AGT TCA GTT GAT ATC AAC AAC TTT GGT GAT Ser Gly Leu Pro Gly Leu Ser Ser Val Asp Ile Asn Asn Phe Gly Asp 480 485 490	1669
55	TCC ATT AAT GAG AGT GAG GGA ATA CCT TTG AAA AGA AGG CGT GTG TCC Ser Ile Asn Glu Ser Glu Gly Ile Pro Leu Lys Arg Arg Arg Val Ser 495 500 505	1717
60	TTT GGT GGG CAC CTA AGA CCT GAA CTA TTT GAT GAA AAC TTG CCT CCT Phe Gly Gly His Leu Arg Pro Glu Leu Phe Asp Glu Asn Leu Pro Pro 510 515 520	1765
65	AAT ACG CCT CTC AAA AGG GGA GAA GCC CCA ACC AAA AGA AAG TCT CTG Asn Thr Pro Leu Lys Arg Gly Glu Ala Pro Thr Lys Arg Lys Ser Leu 525 530 535	1813
70	GTA ATG CAC ACT CCA CCT GTC CTG AAG AAA ATC ATC AAG GAA CAG CCT Val Met His Thr Pro Pro Val Leu Lys Lys Ile Ile Lys Glu Gln Pro 540 545 550 555	1861
75	CAA CCA TCA GGA AAA CAA GAG TCA GGT TCA GAA ATC CAT GTG GAA GTG Gln Pro Ser Gly Lys Gln Glu Ser Gly Ser Glu Ile His Val Glu Val 560 565 570	1909

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	AAG GCA CAA AGC TTG GTT ATA AGC CCT CCA GCT CCT AGT CCT AGG AAA Lys Ala Gln Ser Leu Val Ile Ser Pro Pro Ala Pro Ser Pro Arg Lys 575 580 585	1957
5	ACT CCA GTT GCC AGT GAT CAA CGC CGT AGG TCC TGC AAA ACA GCC CCT Thr Pro Val Ala Ser Asp Gln Arg Arg Ser Cys Lys Thr Ala Pro 590 595 600	2005
10	GCT TCC AGC AGC AAA TCT CAG ACA GAG GTT CCT AAG AGA GGA GGA GAA Ala Ser Ser Ser Lys Ser Gln Thr Glu Val Pro Lys Arg Gly Gly Glu 605 610 615	2053
15	AGA GTG GCA ACC TGC CTT CAA AAG AGA GTG TCT ATC AGC CGA AGT CAA Arg Val Ala Thr Cys Leu Gln Lys Arg Val Ser Ile Ser Arg Ser Gln 620 625 630 635	2101
20	CAT GAT ATT TTA CAG ATG ATA TGT TCC AAA AGA AGA AGT GGT GCT TCG His Asp Ile Leu Gln Met Ile Cys Ser Lys Arg Arg Ser Gly Ala Ser 640 645 650	2149
25	GAA GCA AAT CTG ATT GTT GCA AAA TCA TGG GCA GAT GTA GTA AAA CTT Glu Ala Asn Leu Ile Val Ala Lys Ser Trp Ala Asp Val Val Lys Leu 655 660 665	2197
30	GGT GCA AAA CAA ACA CAA ACT AAA GTC ATA AAA CAT GGT CCT CAA AGG Gly Ala Lys Gln Thr Gln Thr Lys Val Ile Lys His Gly Pro Gln Arg 670 675 680	2245
35	TCA ATG AAC AAA AGG CAA AGA AGA CCT GCT ACT CCA AAG AAG CCT GTG Ser Met Asn Lys Arg Gln Arg Arg Pro Ala Thr Pro Lys Lys Pro Val 685 690 695	2293
40	GGC GAA GTT CAC AGT CAA TTT AGT ACA GGC CAC GCA AAC TCT CCT TGT Gly Glu Val His Ser Gln Phe Ser Thr Gly His Ala Asn Ser Pro Cys 700 705 710 715	2341
45	ACC ATA ATA ATA GGG AAA GCT CAT ACT GAA AAA GTA CAT GTG CCT GCT Thr Ile Ile Ile Gly Lys Ala His Thr Glu Lys Val His Val Pro Ala 720 725 730	2389
50	CGA CCC TAC AGA GTG CTC AAC AAC TTC ATT TCC AAC CAA AAA ATG GAC Arg Pro Tyr Arg Val Leu Asn Asn Phe Ile Ser Asn Gln Lys Met Asp 735 740 745	2437
55	TTT AAG GAA GAT CTT TCA GGA ATA GCT GAA ATG TTC AAG ACC CCA GTG Phe Lys Glu Asp Leu Ser Gly Ile Ala Glu Met Phe Lys Thr Pro Val 750 755 760	2485
60	AAG GAG CAA CCG CAG TTG ACA AGC ACA TGT CAC ATC GCT ATT TCA AAT Lys Glu Gln Pro Gln Leu Thr Ser Thr Cys His Ile Ala Ile Ser Asn 765 770 775	2533
65	TCA GAG AAT TTG CTT GGA AAA CAG TTT CAA GGA ACT GAT TCA GGA GAA Ser Glu Asn Leu Leu Gly Lys Gln Phe Gln Gly Thr Asp Ser Gly Glu 780 785 790 795	2581
	GAA CCT CTG CTC CCC ACC TCA GAG AGT TTT GGA GGA AAT GTG TTC TTC Glu Pro Leu Leu Pro Thr Ser Glu Ser Phe Gly Gly Asn Val Phe Phe 800 805 810	2629
	AGT GCA CAG AAT GCA GCA AAA CAG CCA TCT GAT AAA TGC TCT GCA AGC Ser Ala Gln Asn Ala Ala Lys Gln Pro Ser Asp Lys Cys Ser Ala Ser 815 820 825	2677

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	CCT CCC TTA AGA CGG CAG TGT ATT AGA GAA AAT GGA AAC GTA GCA AAA	2725
	Pro Pro Leu Arg Arg Gln Cys Ile Arg Glu Asn Gly Asn Val Ala Lys	
	830 835 840	
5	ACG CCC AGG AAC ACC TAC AAA ATG ACT TCT CTG GAG ACA AAA ACT TCA	2773
	Thr Pro Arg Asn Thr Tyr Lys Met Thr Ser Leu Glu Thr Lys Thr Ser	
	845 850 855	
10	GAT ACT GAG ACA GAG CCT TCA AAA ACA GTA TCC ACT GTA AAC AGG TCA	2821
	Asp Thr Glu Thr Glu Pro Ser Lys Thr Val Ser Thr Val Asn Arg Ser	
	860 865 870 875	
15	GGA AGG TCT ACA GAG TTC AGG AAT ATA CAG AAG CTA CCT GTG GAA AGT	2869
	Gly Arg Ser Thr Glu Phe Arg Asn Ile Gln Lys Leu Pro Val Glu Ser	
	880 885 890	
20	AAG AGT GAA GAA ACA AAT ACA GAA ATT GTT GAG TGC ATC CTA AAA AGA	2917
	Lys Ser Glu Glu Thr Asn Thr Glu Ile Val Glu Cys Ile Leu Lys Arg	
	895 900 905	
25	GGT CAG AAG GCA ACA CTA CTA CAA CAA AGG AGA GAA GGA GAG ATG AAG	2965
	Gly Gln Lys Ala Thr Leu Leu Gln Gln Arg Arg Glu Gly Glu Met Lys	
	910 915 920	
30	GAA ATA GAA AGA CCT TTT GAG ACA TAT AAG GAA AAT ATT GAA TTA AAA	3013
	Glu Ile Glu Arg Pro Phe Glu Thr Tyr Lys Glu Asn Ile Glu Leu Lys	
	925 930 935	
35	GAA AAC GAT GAA AAG ATG AAA GCA ATG AAG AGA TCA AGA ACT TGG GGG	3061
	Glu Asn Asp Glu Lys Met Lys Ala Met Lys Arg Ser Arg Thr Trp Gly	
	940 945 950 955	
40	CAG AAA TGT GCA CCA ATG TCT GAC CTG ACA GAC CTC AAG AGC TTG CCT	3109
	Gln Lys Cys Ala Pro Met Ser Asp Leu Thr Asp Leu Lys Ser Leu Pro	
	960 965 970	
45	GAT ACA GAA CTC ATG AAA GAC ACG GCA CGT GGC CAG AAT CTC CTC CAA	3157
	Asp Thr Glu Leu Met Lys Asp Thr Ala Arg Gly Gln Asn Leu Leu Gln	
	975 980 985	
50	ACC CAA GAT CAT GCC AAG GCA CCA AAG AGT GAG AAA GGC AAA ATC ACT	3205
	Thr Gln Asp His Ala Lys Ala Pro Lys Ser Glu Lys Gly Lys Ile Thr	
	990 995 1000	
55	AAA ATG CCC TGC CAG TCA TTA CAA CCA GAA CCA ATA AAC ACC CCA ACA	3253
	Lys Met Pro Cys Gln Ser Leu Gln Pro Glu Pro Ile Asn Thr Pro Thr	
	1005 1010 1015	
60	CAC ACA AAA CAA CAG TTG AAG GCA TCC CTG GGG AAA GTA GGT GTG AAA	3301
	His Thr Lys Gln Gln Leu Lys Ala Ser Leu Gly Lys Val Gly Val Lys	
	1020 1025 1030 1035	
65	GAA GAG CTC CTA GCA GTC GGC AAG TTC ACA CGG ACG TCA GGG GAG ACC	3349
	Glu Glu Leu Leu Ala Val Gly Lys Phe Thr Arg Thr Ser Gly Glu Thr	
	1040 1045 1050	
70	ACG CAC ACG CAC AGA GAG CCA GCA GGA GAT GGC AAG AGC ATC AGA ACG	3397
	Thr His Thr His Arg Glu Pro Ala Gly Asp Gly Lys Ser Ile Arg Thr	
	1055 1060 1065	
75	TTT AAG GAG TCT CCA AAG CAG ATC CTG GAC CCA GCA GCC CGT GTA ACT	3445
	Phe Lys Glu Ser Pro Lys Gln Ile Leu Asp Pro Ala Ala Arg Val Thr	
	1070 1075 1080	

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	GGA ATG AAG AAG TGG CCA AGA ACG CCT AAG GAA GAG GCC CAG TCA CTA Gly Met Lys Lys Trp Pro Arg Thr Pro Lys Glu Glu Ala Gln Ser Leu 1085 1090 1095	3493
5	GAA GAC CTG GCT GGC TTC AAA GAG CTC TTC CAG ACA CCA GGT CCC TCT Glu Asp Leu Ala Gly Phe Lys Glu Leu Phe Gln Thr Pro Gly Pro Ser 1100 1105 1110 1115	3541
10	GAG GAA TCA ATG ACT GAT GAG AAA ACT ACC AAA ATA GCC TGC AAA TCT Glu Glu Ser Met Thr Asp Glu Lys Thr Thr Lys Ile Ala Cys Lys Ser 1120 1125 1130	3589
15	CCA CCA CCA GAA TCA GTG GAC ACT CCA ACA AGC ACA AAG CAA TGG CCT Pro Pro Pro Glu Ser Val Asp Thr Pro Thr Ser Thr Lys Gln Trp Pro 1135 1140 1145	3637
20	AAG AGA AGT CTC AGG AAA GCA GAT GTA GAG GAA TTC TTA GCA CTC Lys Arg Ser Leu Arg Lys Ala Asp Val Glu Glu Phe Leu Ala Leu 1150 1155 1160	3685
25	AGG AAA CTA ACA CCA TCA GCA GGG AAA GCC ATG CTT ACG CCC AAA CCA Arg Lys Leu Thr Pro Ser Ala Gly Lys Ala Met Leu Thr Pro Lys Pro 1165 1170 1175	3733
30	GCA GGA GGT GAT GAG AAA GAC ATT AAA GCA TTT ATG GGA ACT CCA GTG Ala Gly Gly Asp Glu Lys Asp Ile Lys Ala Phe Met Gly Thr Pro Val 1180 1185 1190 1195	3781
35	CAG AAA CTG GAC CTG GCA GGA ACT TTA CCT GGC AGC AAA AGA CAG CTA Gln Lys Leu Asp Leu Ala Gly Thr Leu Pro Gly Ser Lys Arg Gln Leu 1200 1205 1210	3829
40	CAG ACT CCT AAG GAA AAG GCC CAG GCT CTA GAA GAC CTG GCT GGC TTT Gln Thr Pro Lys Glu Lys Ala Gln Ala Leu Glu Asp Leu Ala Gly Phe 1215 1220 1225	3877
45	AAA GAG CTC TTC CAG ACT CCT GGT CAC ACC GAG GAA TTA GTG GCT GCT Lys Glu Leu Phe Gln Thr Pro Gly His Thr Glu Glu Leu Val Ala Ala 1230 1235 1240	3925
50	GGT AAA ACC ACT AAA ATA CCC TGC GAC TCT CCA CAG TCA GAC CCA GTG Gly Lys Thr Thr Lys Ile Pro Cys Asp Ser Pro Gln Ser Asp Pro Val 1245 1250 1255	3973
55	GAC ACC CCA ACA AGC ACA AAG CAA CGA CCC AAG AGA AGT ATC AGG AAA Asp Thr Pro Thr Ser Thr Lys Gln Arg Pro Lys Arg Ser Ile Arg Lys 1260 1265 1270 1275	4021
60	GCA GAT GTA GAG GGA GAA CTC TTA GCG TGC AGG AAT CTA ATG CCA TCA Ala Asp Val Glu Gly Glu Leu Leu Ala Cys Arg Asn Leu Met Pro Ser 1280 1285 1290	4069
65	GCA GGC AAA GCC ATG CAC ACG CCT AAA CCA TCA GTC GGT GAA GAG AAA Ala Gly Lys Ala Met His Thr Pro Lys Pro Ser Val Gly Glu Glu Lys 1295 1300 1305	4117
70	GAC ATC ATC ATA TTT GTG GGA ACT CCA GTG CAG AAA CTG GAC CTG ACA Asp Ile Ile Ile Phe Val Gly Thr Pro Val Gln Lys Leu Asp Leu Thr 1310 1315 1320	4165
75	GAG AAC TTA ACC GGC AGC AAG AGA CGG CCA CAA ACT CCT AAG GAA GAG Glu Asn Leu Thr Gly Ser Lys Arg Arg Pro Gln Thr Pro Lys Glu Glu 1325 1330 1335	4213

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	GCC CAG GCT CTG GAA GAC CTG ACT GGC TTT AAA GAG CTC TTC CAG ACC Ala Gln Ala Leu Glu Asp Leu Thr Gly Phe Lys Glu Leu Phe Gln Thr 1340 1345 1350 1355	4261
5	CCT GGT CAT ACT GAA GAA GCA GTG GCT GCT GGC AAA ACT ACT AAA ATG Pro Gly His Thr Glu Glu Ala Val Ala Ala Gly Lys Thr Thr Lys Met 1360 1365 1370	4309
10	CCC TGC GAA TCT TCT CCA CCA GAA TCA GCA GAC ACC CCA ACA AGC ACA Pro Cys Glu Ser Ser Pro Pro Glu Ser Ala Asp Thr Pro Thr Ser Thr 1375 1380 1385	4357
15	AGA AGG CAG CCC AAG ACA CCT TTG GAG AAA AGG GAC GTA CAG AAG GAG Arg Arg Gln Pro Lys Thr Pro Leu Glu Lys Arg Asp Val Gln Lys Glu 1390 1395 1400	4405
20	CTC TCA GCC CTG AAG AAG CTC ACA CAG ACA TCA GGG GAA ACC ACA CAC Leu Ser Ala Leu Lys Lys Leu Thr Gln Thr Ser Gly Glu Thr Thr His 1405 1410 1415	4453
25	ACA GAT AAA GTA CCA GGA GGT GAG GAT AAA AGC ATC AAC GCG TTT AGG Thr Asp Lys Val Pro Gly Gly Glu Asp Lys Ser Ile Asn Ala Phe Arg 1420 1425 1430 1435	4501
30	GAA ACT GCA AAA CAG AAA CTG GAC CCA GCA GCA AGT GTA ACT GGT AGC Glu Thr Ala Lys Gln Lys Leu Asp Pro Ala Ala Ser Val Thr Gly Ser 1440 1445 1450	4549
35	AAG AGG CAC CCA AAA ACT AAG GAA AAG GCC CAA CCC CTA GAA GAC CTG Lys Arg His Pro Lys Thr Lys Glu Lys Ala Gln Pro Leu Glu Asp Leu 1455 1460 1465	4597
40	GCT GGC TGG AAA GAG CTC TTC CAG ACA CCA GTA TGC ACT GAC AAG CCC Ala Gly Trp Lys Glu Leu Phe Gln Thr Pro Val Cys Thr Asp Lys Pro 1470 1475 1480	4645
45	ACG ACT CAC GAG AAA ACT ACC AAA ATA GCC TGC AGA TCA CAA CCA GAC Thr Thr His Glu Lys Thr Thr Lys Ile Ala Cys Arg Ser Gln Pro Asp 1485 1490 1495	4693
50	CCA GTG GAC ACA CCA ACA AGC TCC AAG CCA CAG TCC AAG AGA AGT CTC Pro Val Asp Thr Pro Thr Ser Ser Lys Pro Gln Ser Lys Arg Ser Leu 1500 1505 1510 1515	4741
55	AGG AAA GTG GAC GTA GAA GAA TTC TTC GCA CTC AGG AAA CGA ACA Arg Lys Val Asp Val Glu Glu Phe Phe Ala Leu Arg Lys Arg Thr 1520 1525 1530	4789
60	CCA TCA GCA GGC AAA GCC ATG CAC ACA CCC AAA CCA GCA GTA AGT GGT Pro Ser Ala Gly Lys Ala Met His Thr Pro Lys Pro Ala Val Ser Gly 1535 1540 1545	4837
65	GAG AAA AAC ATC TAC GCA TTT ATG GGA ACT CCA GTG CAG AAA CTG GAC Glu Lys Asn Ile Tyr Ala Phe Met Gly Thr Pro Val Gln Lys Leu Asp 1550 1555 1560	4885
	CTG ACA GAG AAC TTA ACT GGC AGC AAG AGA CGG CTA CAA ACT CCT AAG Leu Thr Glu Asn Leu Thr Gly Ser Lys Arg Arg Leu Gln Thr Pro Lys 1565 1570 1575	4933
	GAA AAG GCC CAG GCT CTA GAA GAC CTG GCT GGC TTT AAA GAG CTC TTC Glu Lys Ala Gln Ala Leu Glu Asp Leu Ala Gly Phe Lys Glu Leu Phe 1580 1585 1590 1595	4981

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	CAG ACA CGA GGT CAC ACT GAG GAA TCA ATG ACT AAC GAT AAA ACT GCC Gln Thr Arg Gly His Thr Glu Glu Ser Met Thr Asn Asp Lys Thr Ala 1600 1605 1610	5029
5	AAA GTA GCC TGC AAA TCT TCA CAA CCA GAC CTA GAC AAA AAC CCA GCA Lys Val Ala Cys Lys Ser Ser Gln Pro Asp Leu Asp Lys Asn Pro Ala 1615 1620 1625	5077
10	AGC TCC AAG CGA CGG CTC AAG ACA TCC CTG GGG AAA GTG GGC GTG AAA Ser Ser Lys Arg Arg Leu Lys Thr Ser Leu Gly Lys Val Gly Val Lys 1630 1635 1640	5125
15	GAA GAG CTC CTA GCA GTT GGC AAG CTC ACA CAG ACA TCA GGA GAG ACT Glu Glu Leu Leu Ala Val Gly Lys Leu Thr Gln Thr Ser Gly Glu Thr 1645 1650 1655	5173
20	ACA CAC ACA CAC ACA GAG CCA ACA GGA GAT GGT AAG AGC ATG AAA GCA Thr His Thr His Thr Glu Pro Thr Gly Asp Gly Lys Ser Met Lys Ala 1660 1665 1670 1675	5221
25	TTT ATG GAG TCT CCA AAG CAG ATC TTA GAC TCA GCA GCA AGT CTA ACT Phe Met Glu Ser Pro Lys Gln Ile Leu Asp Ser Ala Ala Ser Leu Thr 1680 1685 1690	5269
30	GGC AGC AAG AGG CAG CTG AGA ACT CCT AAG GGA AAG TCT GAA GTC CCT Gly Ser Lys Arg Gln Leu Arg Thr Pro Lys Gly Lys Ser Glu Val Pro 1695 1700 1705	5317
35	GAA GAC CTG GCC GGC TTC ATC GAG CTC TTC CAG ACA CCA AGT CAC ACT Glu Asp Leu Ala Gly Phe Ile Glu Leu Phe Gln Thr Pro Ser His Thr 1710 1715 1720	5365
40	AAG GAA TCA ATG ACT AAT GAA AAA ACT ACC AAA GTA TCC TAC AGA GCT Lys Glu Ser Met Thr Asn Glu Lys Thr Thr Lys Val Ser Tyr Arg Ala 1725 1730 1735	5413
45	TCA CAG CCA GAC CTA GTG GAC ACC CCA ACA AGC TCC AAG CCA CAG CCC Ser Gln Pro Asp Leu Val Asp Thr Pro Thr Ser Ser Lys Pro Gln Pro 1740 1745 1750 1755	5461
50	AAG AGA AGT CTC AGG AAA GCA GAC ACT GAA GAA GAA TTT TTA GCA TTT Lys Arg Ser Leu Arg Lys Ala Asp Thr Glu Glu Glu Phe Leu Ala Phe 1760 1765 1770	5509
55	AGG AAA CAA ACG CCA TCA GCA GGC AAA GCC ATG CAC ACA CCC AAA CCA Arg Lys Gln Thr Pro Ser Ala Gly Lys Ala Met His Thr Pro Lys Pro 1775 1780 1785	5557
60	GCA GTA GGT GAA GAG AAA GAC ATC AAC ACG TTT TTG GGA ACT CCA GTG Ala Val Gly Glu Glu Lys Asp Ile Asn Thr Phe Leu Gly Thr Pro Val 1790 1795 1800	5605
65	CAG AAA CTG GAC CAG CCA GGA AAT TTA CCT GGC AGC AAT AGA CGG CTA Gln Lys Leu Asp Gln Pro Gly Asn Leu Pro Gly Ser Asn Arg Arg Leu 1805 1810 1815	5653
70	CAA ACT CGT AAG GAA AAG GCC CAG GCT CTA GAA GAA CTG ACT GGC TTC Gln Thr Arg Lys Glu Lys Ala Gln Ala Leu Glu Glu Leu Thr Gly Phe 1820 1825 1830 1835	5701
75	AGA GAG CTT TTC CAG ACA CCA TGC ACT GAT AAC CCC ACA GCT GAT GAG Arg Glu Leu Phe Gln Thr Pro Cys Thr Asp Asn Pro Thr Ala Asp Glu 1840 1845 1850	5749

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	AAA ACT ACC AAA AAA ATA CTC TGC AAA TCT CCG CAA TCA GAC CCA GCG Lys Thr Thr Lys Lys Ile Leu Cys Lys Ser Pro Gln Ser Asp Pro Ala 1855 1860 1865	5797
5	GAC ACC CCA ACA AAC ACA AAG CAA CGG CCC AAG AGA AGC CTC AAG AAA Asp Thr Pro Thr Asn Thr Lys Gln Arg Pro Lys Arg Ser Leu Lys Lys 1870 1875 1880	5845
10	GCA GAC GTA GAG GAA TTT TTA GCA TTC AGG AAA CTA ACA CCA TCA Ala Asp Val Glu Glu Phe Leu Ala Phe Arg Lys Leu Thr Pro Ser 1885 1890 1895	5893
15	GCA GGC AAA GCC ATG CAC ACG CCT AAA GCA GCA GTA GGT GAA GAG AAA Ala Gly Lys Ala Met His Thr Pro Lys Ala Ala Val Gly Glu Glu Lys 1900 1905 1910 1915	5941
	GAC ATC AAC ACA TTT GTG GGG ACT CCA GTG GAG AAA CTG GAC CTG CTA Asp Ile Asn Thr Phe Val Gly Thr Pro Val Glu Lys Leu Asp Leu Leu 1920 1925 1930	5989
20	GGA AAT TTA CCT GGC AGC AAG AGA CGG CCA CAA ACT CCT AAA GAA AAG Gly Asn Leu Pro Gly Ser Lys Arg Arg Pro Gln Thr Pro Lys Glu Lys 1935 1940 1945	6037
25	GCC AAG GCT CTA GAA GAT CTG GCT GGC TTC AAA GAG CTC TTC CAG ACA Ala Lys Ala Leu Glu Asp Leu Ala Gly Phe Lys Glu Leu Phe Gln Thr 1950 1955 1960	6085
30	CCA GGT CAC ACT GAG GAA TCA ATG ACC GAT GAC AAA ATC ACA GAA GTA Pro Gly His Thr Glu Glu Ser Met Thr Asp Asp Lys Ile Thr Glu Val 1965 1970 1975	6133
35	TCC TGC AAA TCT CCA CAA CCA GAC CCA GTC AAA ACC CCA ACA AGC TCC Ser Cys Lys Ser Pro Gln Pro Asp Pro Val Lys Thr Pro Thr Ser Ser 1980 1985 1990 1995	6181
	AAG CAA CGA CTC AAG ATA TCC TTG GGG AAA GTA GGT GTG AAA GAA GAG Lys Gln Arg Leu Lys Ile Ser Leu Gly Lys Val Gly Val Lys Glu Glu 2000 2005 2010	6229
40	GTC CTA CCA GTC GGC AAG CTC ACA CAG ACG TCA GGG AAG ACC ACA CAG Val Leu Pro Val Gly Lys Leu Thr Gln Thr Ser Gly Lys Thr Thr Gln 2015 2020 2025	6277
45	ACA CAC AGA GAG ACA GCA GGA GAT GGA AAG AGC ATC AAA GCG TTT AAG Thr His Arg Glu Thr Ala Gly Asp Gly Lys Ser Ile Lys Ala Phe Lys 2030 2035 2040	6325
50	GAA TCT GCA AAG CAG ATG CTG GAC CCA GCA AAC TAT GGA ACT GGG ATG Glu Ser Ala Lys Gln Met Leu Asp Pro Ala Asn Tyr Gly Thr Gly Met 2045 2050 2055	6373
55	GAG AGG TGG CCA AGA ACA CCT AAG GAA GAG GCC CAA TCA CTA GAA GAC Glu Arg Trp Pro Arg Thr Pro Lys Glu Ala Gln Ser Leu Glu Asp 2060 2065 2070 2075	6421
	CTG GCC GGC TTC AAA GAG CTC TTC CAG ACA CCA GAC CAC ACT GAG GAA Leu Ala Gly Phe Lys Glu Leu Phe Gln Thr Pro Asp His Thr Glu Glu 2080 2085 2090	6469
60	TCA ACA ACT GAT GAC AAA ACT ACC AAA ATA GCC TGC AAA TCT CCA CCA Ser Thr Thr Asp Asp Lys Thr Thr Lys Ile Ala Cys Lys Ser Pro Pro 2095 2100 2105	6517

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	CCA GAA TCA ATG GAC ACT CCA ACA AGC ACA AGG AGG CGG CCC AAA ACA Pro Glu Ser Met Asp Thr Pro Thr Ser Thr Arg Arg Arg Pro Lys Thr 2110 2115 2120	6565
5	CCT TTG GGG AAA AGG GAT ATA GTG GAA GAG CTC TCA GCC CTG AAG CAG Pro Leu Gly Lys Arg Asp Ile Val Glu Glu Leu Ser Ala Leu Lys Gln 2125 2130 2135	6613
10	CTC ACA CAG ACC ACA CAC ACA GAC AAA GTA CCA GGA GAT GAG GAT AAA Leu Thr Gln Thr Thr His Thr Asp Lys Val Pro Gly Asp Glu Asp Lys 2140 2145 2150 2155	6661
15	GGC ATC AAC GTG TTC AGG GAA ACT GCA AAA CAG AAA CTG GAC CCA GCA Gly Ile Asn Val Phe Arg Glu Thr Ala Lys Gln Lys Leu Asp Pro Ala 2160 2165 2170	6709
20	GCA AGT GTA ACT GGT AGC AAG AGG CAG CCA AGA ACT CCT AAG GGA AAA Ala Ser Val Thr Gly Ser Lys Arg Gln Pro Arg Thr Pro Lys Gly Lys 2175 2180 2185	6757
25	GCC CAA CCC CTA GAA GAC TTG GCT GGC TTG AAA GAG CTC TTC CAG ACA Ala Gln Pro Leu Glu Asp Leu Ala Gly Leu Lys Glu Leu Phe Gln Thr 2190 2195 2200	6805
30	CCA GTA TGC ACT GAC AAG CCC ACG ACT CAC GAG AAA ACT ACC AAA ATA Pro Val Cys Thr Asp Lys Pro Thr Thr His Glu Lys Thr Thr Lys Ile 2205 2210 2215	6853
35	GCC TGC AGA TCT CCA CAA CCA GAC CCA GTG GGT ACC CCA ACA ATC TTC Ala Cys Arg Ser Pro Gln Pro Asp Pro Val Gly Thr Pro Thr Ile Phe 2220 2225 2230 2235	6901
40	AAG CCA CAG TCC AAG AGA AGT CTC AGG AAA GCA GAC GTA GAG GAA GAA Lys Pro Gln Ser Lys Arg Ser Leu Arg Lys Ala Asp Val Glu Glu Glu 2240 2245 2250	6949
45	TCC TTA GCA CTC AGG AAA CGA ACA CCA TCA GTA GGG AAA GCT ATG GAC Ser Leu Ala Leu Arg Lys Arg Thr Pro Ser Val Gly Lys Ala Met Asp 2255 2260 2265	6997
50	ACA CCC AAA CCA GCA GGA GGT GAT GAG AAA GAC ATG AAA GCA TTT ATG Thr Pro Lys Pro Ala Gly Gly Asp Glu Lys Asp Met Lys Ala Phe Met 2270 2275 2280	7045
55	GGA ACT CCA GTG CAG AAA TTG GAC CTG CCA GGA AAT TTA CCT GGC AGC Gly Thr Pro Val Gln Lys Leu Asp Leu Pro Gly Asn Leu Pro Gly Ser 2285 2290 2295	7093
60	AAA AGA TGG CCA CAA ACT CCT AAG GAA AAG GCC CAG GCT CTA GAA GAC Lys Arg Trp Pro Gln Thr Pro Lys Glu Lys Ala Gln Ala Leu Glu Asp 2300 2305 2310 2315	7141
65	CTG GCT GGC TTC AAA GAG CTC TTC CAG ACA CCA GGC ACT GAC AAG CCC Leu Ala Gly Phe Lys Glu Leu Phe Gln Thr Pro Gly Thr Asp Lys Pro 2320 2325 2330	7189
70	ACG ACT GAT GAG AAA ACT ACC AAA ATA GCC TGC AAA TCT CCA CAA CCA Thr Thr Asp Glu Lys Thr Lys Ile Ala Cys Lys Ser Pro Gln Pro 2335 2340 2345	7237
75	GAC CCA GTG GAC ACC CCA GCA AGC ACA AAG CAA CGG CCC AAG AGA AAC Asp Pro Val Asp Thr Pro Ala Ser Thr Lys Gln Arg Pro Lys Arg Asn 2350 2355 2360	7285

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	CTC AGG AAA GCA GAC GTA GAG GAA GAA TTT TTA GCA CTC AGG AAA CGA Leu Arg Lys Ala Asp Val Glu Glu Glu Phe Leu Ala Leu Arg Lys Arg 2365 2370 2375	7333
5	ACA CCA TCA GCA GGC AAA GCC ATG GAC ACC CCA AAA CCA GCA GTA AGT Thr Pro Ser Ala Gly Lys Ala Met Asp Thr Pro Lys Pro Ala Val Ser 2380 2385 2390 2395	7381
10	GAT GAG AAA AAT ATC AAC ACA TTT GTG GAA ACT CCA GTG CAG AAA CTG Asp Glu Lys Asn Ile Asn Thr Phe Val Glu Thr Pro Val Gln Lys Leu 2400 2405 2410	7429
15	GAC CTG CTA GGA AAT TTA CCT GGC AGC AAG AGA CAG CCA CAG ACT CCT Asp Leu Leu Gly Asn Leu Pro Gly Ser Lys Arg Gln Pro Gln Thr Pro 2415 2420 2425	7477
20	AAG GAA AAG GCT GAG GCT CTA GAG GAC CTG GTT GGC TTC AAA GAA CTC Lys Glu Lys Ala Glu Ala Leu Glu Asp Leu Val Gly Phe Lys Glu Leu 2430 2435 2440	7525
25	TTC CAG ACA CCA GGT CAC ACT GAG GAA TCA ATG ACT GAT GAC AAA ATC Phe Gln Thr Pro Gly His Thr Glu Glu Ser Met Thr Asp Asp Lys Ile 2445 2450 2455	7573
30	ACA GAA GTA TCC TGT AAA TCT CCA CAG CCA GAG TCA TTC AAA ACC TCA Thr Glu Val Ser Cys Lys Ser Pro Gln Pro Glu Ser Phe Lys Thr Ser 2460 2465 2470 2475	7621
35	AGA AGC TCC AAG CAA AGG CTC AAG ATA CCC CTG GTG AAA GTG GAC ATG Arg Ser Ser Lys Gln Arg Leu Lys Ile Pro Leu Val Lys Val Asp Met 2480 2485 2490	7669
40	AAA GAA GAG CCC CTA GCA GTC AGC AAG CTC ACA CGG ACA TCA GGG GAG Lys Glu Glu Pro Leu Ala Val Ser Lys Leu Thr Arg Thr Ser Gly Glu 2495 2500 2505	7717
45	ACT ACG CAA ACA CAC ACA GAG CCA ACA GGA GAT AGT AAG AGC ATC AAA Thr Thr Gln Thr His Thr Glu Pro Thr Gly Asp Ser Lys Ser Ile Lys 2510 2515 2520	7765
50	GCG TTT AAG GAG TCT CCA AAG CAG ATC CTG GAC CCA GCA GCA AGT GTA Ala Phe Lys Glu Ser Pro Lys Gln Ile Leu Asp Pro Ala Ala Ser Val 2525 2530 2535	7813
55	ACT GGT AGC AGG AGG CAG CTG AGA ACT CGT AAG GAA AAG GCC CGT GCT Thr Gly Ser Arg Arg Gln Leu Arg Thr Arg Lys Glu Lys Ala Arg Ala 2540 2545 2550 2555	7861
60	CTA GAA GAC CTG GTT GAC TTC AAA GAG CTC TTC TCA GCA CCA GGT CAC Leu Glu Asp Leu Val Asp Phe Lys Glu Leu Phe Ser Ala Pro Gly His 2560 2565 2570	7909
65	ACT GAA GAG TCA ATG ACT ATT GAC AAA AAC ACA AAA ATT CCC TGC AAA Thr Glu Glu Ser Met Thr Ile Asp Lys Asn Thr Lys Ile Pro Cys Lys 2575 2580 2585	7957
	TCT CCC CCA CCA GAA CTA ACA GAC ACT GCC ACG AGC ACA AAG AGA TGC Ser Pro Pro Pro Glu Leu Thr Asp Thr Ala Thr Ser Thr Lys Arg Cys 2590 2595 2600	8005
	CCC AAG ACA CGT CCC AGG AAA GAA GTA AAA GAG GAG CTC TCA GCA GTT Pro Lys Thr Arg Pro Arg Lys Glu Val Lys Glu Glu Leu Ser Ala Val 2605 2610 2615	8053

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	GAG AGG CTC ACG CAA ACA TCA GGG CAA AGC ACA CAC ACA CAC AAA GAA Glu Arg Leu Thr Gln Thr Ser Gly Gln Ser Thr His Thr His Lys Glu 2620 2625 2630 2635	8101
• 5	CCA GCA AGC GGT GAT GAG GGC ATC AAA GTA TTG AAG CAA CGT GCA AAG Pro Ala Ser Gly Asp Glu Gly Ile Lys Val Leu Lys Gln Arg Ala Lys 2640 2645 2650	8149
10	AAG AAA CCA AAC CCA GTA GAA GAG GAA CCC AGC AGG AGA AGG CCA AGA Lys Lys Pro Asn Pro Val Glu Glu Pro Ser Arg Arg Arg Pro Arg 2655 2660 2665	8197
15	GCA CCT AAG GAA AAG GCC CAA CCC CTG GAA GAC CTG GCC GGC TTC ACA Ala Pro Lys Glu Lys Ala Gln Pro Leu Glu Asp Leu Ala Gly Phe Thr 2670 2675 2680	8245
20	GAG CTC TCT GAA ACA TCA GGT CAC ACT CAG GAA TCA CTG ACT GCT GGC Glu Leu Ser Glu Thr Ser Gly His Thr Gln Glu Ser Leu Thr Ala Gly 2685 2690 2695	8293
25	AAA GCC ACT AAA ATA CCC TGC GAA TCT CCC CCA CTA GAA GTG GTA GAC Lys Ala Thr Lys Ile Pro Cys Glu Ser Pro Pro Leu Glu Val Val Asp 2700 2705 2710 2715	8341
30	ACC ACA GCA AGC ACA AAG AGG CAT CTC AGG ACA CGT GTG CAG AAG GTA Thr Thr Ala Ser Thr Lys Arg His Leu Arg Thr Arg Val Gln Lys Val 2720 2725 2730	8389
35	CAA GTA AAA GAA GAG CCT TCA GCA GTC AAG TTC ACA CAA ACA TCA GGG Gln Val Lys Glu Glu Pro Ser Ala Val Lys Phe Thr Gln Thr Ser Gly 2735 2740 2745	8437
40	GAA ACC ACG GAT GCA GAC AAA GAA CCA GCA GGT GAA GAT AAA GGC ATC Glu Thr Thr Asp Ala Asp Lys Glu Pro Ala Gly Glu Asp Lys Gly Ile 2750 2755 2760	8485
45	AAA GCA TTG AAG GAA TCT GCA AAA CAG ACA CCG GCT CCA GCA GCA AGT Lys Ala Leu Lys Glu Ser Ala Lys Gln Thr Pro Ala Pro Ala Ala Ser 2765 2770 2775	8533
50	GTA ACT GGC AGC AGG AGA CGG CCA AGA GCA CCC AGG GAA AGT GCC CAA Val Thr Gly Ser Arg Arg Pro Arg Ala Pro Arg Glu Ser Ala Gln 2780 2785 2790 2795	8581
55	GCC ATA GAA GAC CTA GCT GGC TTC AAA GAC CCA GCA GCA GGT CAC ACT Ala Ile Glu Asp Leu Ala Gly Phe Lys Asp Pro Ala Ala Gly His Thr 2800 2805 2810	8629
60	GAA GAA TCA ATG ACT GAT GAC AAA ACC ACT AAA ATA CCC TGC AAA TCA Glu Glu Ser Met Thr Asp Asp Lys Thr Thr Lys Ile Pro Cys Lys Ser 2815 2820 2825	8677
65	TCA CCA GAA CTA GAA GAC ACC GCA ACA AGC TCA AAG AGA CGG CCC AGG Ser Pro Glu Leu Glu Asp Thr Ala Thr Ser Ser Lys Arg Arg Pro Arg 2830 2835 2840	8725
	ACA CGT GCC CAG AAA GTA GAA GTG AAG GAG GAG CTG TTA GCA GTT GGC Thr Arg Ala Gln Lys Val Glu Val Lys Glu Leu Leu Ala Val Gly 2845 2850 2855	8773
	AAG CTC ACA CAA ACC TCA GGG GAG ACC ACG CAC ACC GAC AAA GAG CCG Lys Leu Thr Gln Thr Ser Gly Glu Thr Thr His Thr Asp Lys Glu Pro 2860 2865 2870 2875	8821

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	GTA GGT GAG GGC AAA GGC ACG AAA GCA TTT AAG CAA CCT GCA AAG CGG Val Gly Glu Gly Lys Gly Thr Lys Ala Phe Lys Gln Pro Ala Lys Arg 2880 2885 2890	8869
5	AAC GTG GAC GCA GAA GAT GTA ATT GGC AGC AGG AGA CAG CCA AGA GCA Asn Val Asp Ala Glu Asp Val Ile Gly Ser Arg Arg Gln Pro Arg Ala 2895 2900 2905	8917
10	CCT AAG GAA AAG GCC CAA CCC CTG GAA GAC CTG GCC AGC TTC CAA GAG Pro Lys Glu Lys Ala Gln Pro Leu Glu Asp Leu Ala Ser Phe Gln Glu 2910 2915 2920	8965
15	CTC TCT CAA ACA CCA GGC CAC ACT GAG GAA CTG GCA AAT GGT GCT GCT Leu Ser Gln Thr Pro Gly His Thr Glu Glu Leu Ala Asn Gly Ala Ala 2925 2930 2935	9013
20	GAT AGC TTT ACA AGC GCT CCA AAG CAA ACA CCT GAC AGT GGA AAA CCT Asp Ser Phe Thr Ser Ala Pro Lys Gln Thr Pro Asp Ser Gly Lys Pro 2940 2945 2950 2955	9061
25	CTA AAA ATA TCC AGA AGA GTT CTT CGG GCC CCT AAA GTA GAA CCC GTG Leu Lys Ile Ser Arg Arg Val Leu Arg Ala Pro Lys Val Glu Pro Val 2960 2965 2970	9109
30	GGA GAC GTG GTA AGC ACC AGA GAC CCT GTA AAA TCA CAA AGC AAA AGC Gly Asp Val Val Ser Thr Arg Asp Pro Val Lys Ser Gln Ser Lys Ser 2975 2980 2985	9157
35	AAC ACT TCC CTG CCC CCA CTG CCC TTC AAG AGG GGA GGT GGC AAA GAT Asn Thr Ser Leu Pro Pro Leu Pro Phe Lys Arg Gly Gly Lys Asp 2990 2995 3000	9205
40	GGA AGC GTC ACG GGA ACC AAG AGG CTG CGC TGC ATG CCA GCA CCA GAG Gly Ser Val Thr Gly Thr Lys Arg Leu Arg Cys Met Pro Ala Pro Glu 3005 3010 3015	9253
45	GAA ATT GTG GAG GAG CTG CCA GCC AGC AAG AAG CAG AGG GTT GCT CCC Glu Ile Val Glu Glu Leu Pro Ala Ser Lys Lys Gln Arg Val Ala Pro 3020 3025 3030 3035	9301
50	AGG GCA AGA GGC AAA TCA TCC GAA CCC GTG GTC ATC ATG AAG AGA AGT Arg Ala Arg Gly Lys Ser Ser Glu Pro Val Val Ile Met Lys Arg Ser 3040 3045 3050	9349
55	TTG AGG ACT TCT GCA AAA AGA ATT GAA CCT GCG GAA GAG CTG AAC AGC Leu Arg Thr Ser Ala Lys Arg Ile Glu Pro Ala Glu Glu Leu Asn Ser 3055 3060 3065	9397
60	AAC GAC ATG AAA ACC AAC AAA GAG GAA CAC AAA TTA CAA GAC TCG GTC Asn Asp Met Lys Thr Asn Lys Glu Glu His Lys Leu Gln Asp Ser Val 3070 3075 3080	9445
65	CCT GAA AAT AAG GGA ATA TCC CTG CGC TCC AGA CGC CAA GAT AAG ACT Pro Glu Asn Lys Gly Ile Ser Leu Arg Ser Arg Arg Gln Asp Lys Thr 3085 3090 3095	9493
70	GAG GCA GAA CAG CAA ATA ACT GAG GTC TTT GTA TTA GCA GAA AGA ATA Glu Ala Glu Gln Gln Ile Thr Glu Val Phe Val Leu Ala Glu Arg Ile 3100 3105 3110 3115	9541
75	GAA ATA AAC AGA AAT GAA AAG AAG CCC ATG AAG ACC TCC CCA GAG ATG Glu Ile Asn Arg Asn Glu Lys Lys Pro Met Lys Thr Ser Pro Glu Met 3120 3125 3130	9589

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	GAC ATT CAG AAT CCA GAT GAT GGA GCC CGG AAA CCC ATA CCT AGA GAC Asp Ile Gln Asn Pro Asp Asp Gly Ala Arg Lys Pro Ile Pro Arg Asp 3135 3140 3145	9637
5	AAA GTC ACT GAG AAC AAA AGG TGC TTG AGG TCT GCT AGA CAG AAT GAG Lys Val Thr Glu Asn Lys Arg Cys Leu Arg Ser Ala Arg Gln Asn Glu 3150 3155 3160	9685
10	AGC TCC CAG CCT AAG GTG GCA GAG GAG AGC GGA GGG CAG AAG AGT GCG Ser Ser Gln Pro Lys Val Ala Glu Glu Ser Gly Gly Gln Lys Ser Ala 3165 3170 3175	9733
15	AAG GTT CTC ATG CAG AAT CAG AAA GGG AAA GGA GAA GCA GGA AAT TCA Lys Val Leu Met Gln Asn Gln Lys Gly Lys Gly Glu Ala Gly Asn Ser 3180 3185 3190 3195	9781
20	GAC TCC ATG TGC CTG AGA TCA AGA AAG ACA AAA AGC CAG CCT GCA GCA Asp Ser Met Cys Leu Arg Ser Arg Lys Thr Lys Ser Gln Pro Ala Ala 3200 3205 3210	9829
25	AGC ACT TTG GAG AGC AAA TCT GTG CAG AGA GTA ACG CGG AGT GTC AAG Ser Thr Leu Glu Ser Lys Ser Val Gln Arg Val Thr Arg Ser Val Lys 3215 3220 3225	9877
30	AGG TGT GCA GAA AAT CCA AAG AAG GCT GAG GAC AAT GTG TGT GTC AAG Arg Cys Ala Glu Asn Pro Lys Lys Ala Glu Asp Asn Val Cys Val Lys 3230 3235 3240	9925
35	AAA ATA ACA ACC AGA AGT CAT AGG GAC AGT GAA GAT ATT TGACAGAAAA Lys Ile Thr Thr Arg Ser His Arg Asp Ser Glu Asp Ile 3245 3250 3255 <i>qqst</i>	9974
40	ATCGAACTGG GAAAAATATA ATAAAGTTAG TTTTGATA AGTTCTAGTG CAGTTTTGT CATAAAATTAC AAGTGAATTG TGTAAGTAAG GCTGTCAGTC TGCTTAAGGG AAGAAAACCT TGGATTGCT GGGCTGAAT CGGCTTCATA AACTCCACTG GGAGCACTGC TGGGCTCCTG GACTGAGAAT AGTTGAACAC CGGGGGCTTT GTGAAGGAGT CTGGGCCAAG GTTGGCCCTC AGCTTTGCAG AATGAAGCCT TGAGGTCTGT CACCACCCAC AGCCACCCCTA CAGCAGCCTT AACTGTGACA CTTGCCACAC TGTGTCGTCG TTTGTTGCC TATGTTCTCC AGGGCACGGT GGCAGGAACA ACTATCCTCG TCTGTCCCAA CACTGAGCAG GCACCTGGTA AACACGAATG AATGGATAAG CGCACGGATG AATGGAGCTT ACAAGATCTG TCTTCCAAT GGCGGGGGC ATTTGGTCCC CAAATTAAGG CTATTGACA TCTGCACAGG ACAGTCCTAT TTTTGATGTC CTTTCCTTTC TGAAAATAAA GTTTGTGCT TTGGAGAATG ACTCGTGAGC ACATCTTAG GGACCAAGAG TGACTTCTG TAAGGAGTGA CTCGTGGCTT GCCTTGGTCT CTTGGGAATA CTTTCTAAC TAGGGTTGCT CTCACCTGAG ACATTCTCCA CCCGCCGAAT CTCAGGGTCC CAGGCTGTGG GCCATCACGA CCTCAAAC TG GCTCCTAAC TCCAGCTTC CTGTCATTGA AAGCTTCGGA AGTTTACTGG CTCTGCTCCC GCCTGTTTC TTTCTGACTC TATCTGGCAG 60 CCCGATGCCA CCCAGTACAG GAAGTGACAC CAGTACTCTG TAAAGCATCA TCATCCTTGG AGAGACTGAG CACTCAGCAC CTTCAGCCAC GATTCAGGA TCGCTTCCTT GTGAGCCGCT 65	10034 10094 10154 10214 10274 10334 10394 10454 10514 10574 10634 10694 10754 10814 10874 10934

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	GCCTCCGAAA TCTCCTTGA AGCCCAGACA TCTTCCTCCA GCTTCAGACT TGTAGATATA	10994
	ACTCGTTCAT CTTCATTTAC TTTCCACTTT GCCCCCTGTC CTCTCTGTGT TCCCCAAATC	11054
5	AGAGAATAGC CCGCCATCCC CCAGATCACC TGTCTGGATT CCTCCCCATT CACCCACCTT	11114
	GCCAGGTGCA GGTGAGGATG GTGCACCAGA CAGGGTAGCT GTCCCCAAA ATGTGCCCTG	11174
	TGCGGGCAGT GCCCTGTCTC CACGTTGTT TCCCCAGTGT CTGGCGGGGA GCCAGGTGAC	11234
10	ATCATAAATA CTTGCTGAAT GAATGCAGAA ATCAGCGGTA CTGACTTGTA CTATATTGGC	11294
	TGCCATGATA GGGTTCTCAC AGCGTCATCC ATGATCGTAA GGGAGAATGA CATTCTGCTT	11354
15	GAGGGAGGGA ATAGAAAGGG GCAGGGAGGG GACATCTGAG GGCTTCACAG GGCTGCAAAG	11414
	GGTACAGGGA TTGCACCAGG GCAGAACAGG GGAGGGTGT CAAGGAAGAG TGGCTCTAG	11474
	CAGAGGCACT TTGGAAGGTG TGAGGCATAA ATGCTTCCTT CTACGTAGGC CAACCTCAAA	11534
20	ACTTTCAGTA GGAATGTTGC TATGATCAAG TTGTTCTAAC ACTTTAGACT TAGTAGTAAT	11594
	TATGAACCTC ACATAGAAAA ATTCATCCA GCCATATGCC TGTGGAGTGG AATATTCTGT	11654
25	TTAGTAGAAA AATCCTTCTAG AGTCAGCTC TAACCAGAAA TCTTGCTGAA GTATGTCAGC	11714
	ACCTTTCTC ACCCTGGTAA GTACAGTATT TCAAGAGCAC GCTAAGGGTG GTTTTCATTT	11774
	TACAGGGCTG TTGATGATGG GTTAAAAATG TTCATTTAAG GGCTACCCCC GTGTTTAATA	11834
30	GATGAACACC ACTTCTACAC AACCCCTCCTT GGTACTGGGG GAGGGAGAGA TCTGACAAAT	11894
	ACTGCCATT CCCCTAGGCT GACTGGATT GAGAACAAAT ACCCACCCAT TTCCACCATG	11954
35	GTATGGTAAC TTCTCTGAGC TTCAGTTCC AAGTGAATT CCATGTAATA GGACATCCCC	12014
	ATTAAATACA AGCTGTTTT ACTTTTCGC CTCCCAGGGC CTGTGCGATC TGGTCCCCCA	12074
	GCCTCTCTTG GGCTTCTTA CACTAACTCT GTACCTACCA TCTCCTGCCT CCCTTAGGCA	12134
40	GGCACCTCCA ACCACCACAC ACTCCCTGCT GTTTCCCTG CCTGGAACCT TCCCACCAGC	12194
	CCCACCAAGA TCATTTCATC CAGTCCTGAG CTCAGCTTAA GGGAGGCTTC TTGCCTGTGG	12254
45	GTTCCCTCAC CCCCATGCCT GTCCTCCAGG CTGGGGCAGG TTCTTAGTT GCCTGGAATT	12314
	GTTCTGTACC TCTTGTTAGC ACGTAGTGT GTGAAACTAA GCCACTAATT GAGTTCTGG	12374
	CTCCCCCTCCT GGGTTGTAA GTTTGTTCA TTCATGAGGG CCGACTGTAT TTCCTGGTTA	12434
50	CTGTATCCCA GTGACCAGCC ACAGGAGATG TCCAATAAAG TATGTGATGA AATGGTCTT	12493

(2) INFORMATION FOR SEQ ID NO: 2:

- 55 (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3256 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- 60 (ii) MOLECULE TYPE: Protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

65	Met Trp Pro Thr Arg Arg Leu Val Thr Ile Lys Arg Ser Gly Val Asp
	1 5 10 15

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	Gly	Pro	His	Phe	Pro	Leu	Ser	Leu	Ser	Thr	Cys	Leu	Phe	Gly	Arg	Gly
				20					25					30		
5	Ile	Glu	Cys	Asp	Ile	Arg	Ile	Gln	Leu	Pro	Val	Val	Ser	Lys	Gln	His
		35						40					45			
	Cys	Lys	Val	Glu	Ile	His	Glu	Gln	Glu	Ala	Ile	Leu	His	Asn	Phe	Ser
		50					55					60				
10	Ser	Thr	Asn	Pro	Thr	Gln	Val	Asn	Gly	Ser	Val	Ile	Asp	Glu	Pro	Val
		65				70				75			80			
	Arg	Leu	Lys	His	Gly	Asp	Val	Ile	Thr	Ile	Ile	Asp	Arg	Ser	Phe	Arg
			85					90					95			
15	Tyr	Glu	Asn	Glu	Ser	Leu	Gln	Asn	Gly	Arg	Lys	Ser	Thr	Glu	Phe	Pro
		100					105						110			
20	Arg	Lys	Ile	Arg	Glu	Gln	Glu	Pro	Ala	Arg	Arg	Val	Ser	Arg	Ser	Ser
		115					120					125				
	Phe	Ser	Ser	Asp	Pro	Asp	Glu	Lys	Ala	Gln	Asp	Ser	Lys	Ala	Tyr	Ser
		130				135						140				
25	Lys	Ile	Thr	Glu	Gly	Lys	Val	Ser	Gly	Asn	Pro	Gln	Val	His	Ile	Lys
	145				150					155				160		
	Asn	Val	Lys	Glu	Asp	Ser	Thr	Ala	Asp	Asp	Ser	Lys	Asp	Ser	Val	Ala
			165					170					175			
30	Gln	Gly	Thr	Thr	Asn	Val	His	Ser	Ser	Glu	His	Ala	Gly	Arg	Asn	Gly
		180					185						190			
35	Arg	Asn	Ala	Ala	Asp	Pro	Ile	Ser	Gly	Asp	Phe	Lys	Glu	Ile	Ser	Ser
		195					200					205				
	Val	Lys	Leu	Val	Ser	Arg	Tyr	Gly	Glu	Leu	Lys	Ser	Val	Pro	Thr	Thr
		210				215						220				
40	Gln	Cys	Leu	Asp	Asn	Ser	Lys	Lys	Asn	Glu	Ser	Pro	Phe	Trp	Lys	Leu
	225				230					235			240			
	Tyr	Glu	Ser	Val	Lys	Lys	Glu	Leu	Asp	Val	Lys	Ser	Gln	Lys	Glu	Asn
		245				250							255			
45	Val	Leu	Gln	Tyr	Cys	Arg	Lys	Ser	Gly	Leu	Gln	Thr	Asp	Tyr	Ala	Thr
		260				265							270			
50	Glu	Lys	Glu	Ser	Ala	Asp	Gly	Leu	Gln	Gly	Glu	Thr	Gln	Leu	Leu	Val
		275				280							285			
	Ser	Arg	Lys	Ser	Arg	Pro	Lys	Ser	Gly	Gly	Ser	Gly	His	Ala	Val	Ala
		290				295						300				
55	Glu	Pro	Ala	Ser	Pro	Glu	Gln	Glu	Leu	Asp	Gln	Asn	Lys	Gly	Lys	Gly
	305				310					315			320			
	Arg	Asp	Val	Glu	Ser	Val	Gln	Thr	Pro	Ser	Lys	Ala	Val	Gly	Ala	Ser
		325				330							335			
60	Phe	Pro	Leu	Tyr	Glu	Pro	Ala	Lys	Met	Lys	Thr	Pro	Val	Gln	Tyr	Ser
		340				345							350			

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	Gln	Gln	Gln	Asn	Ser	Pro	Gln	Lys	His	Lys	Asn	Lys	Asp	Leu	Tyr	Thr
	355						360					365				
5	Thr	Gly	Arg	Arg	Glu	Ser	Val	Asn	Leu	Gly	Lys	Ser	Glu	Gly	Phe	Lys
	370				375					380						
	Ala	Gly	Asp	Lys	Thr	Leu	Thr	Pro	Arg	Lys	Leu	Ser	Thr	Arg	Asn	Arg
	385				390					395				400		
10	Thr	Pro	Ala	Lys	Val	Glu	Asp	Ala	Ala	Asp	Ser	Ala	Thr	Lys	Pro	Glu
	405							410					415			
	Asn	Leu	Ser	Ser	Lys	Thr	Arg	Gly	Ser	Ile	Pro	Thr	Asp	Val	Glu	Val
	420							425					430			
15	Leu	Pro	Thr	Glu	Thr	Glu	Ile	His	Asn	Glu	Pro	Phe	Leu	Thr	Leu	Trp
	435						440					445				
20	Leu	Thr	Gln	Val	Glu	Arg	Lys	Ile	Gln	Lys	Asp	Ser	Leu	Ser	Lys	Pro
	450						455					460				
	Glu	Lys	Leu	Gly	Thr	Thr	Ala	Gly	Gln	Met	Cys	Ser	Gly	Leu	Pro	Gly
	465						470				475				480	
25	Leu	Ser	Ser	Val	Asp	Ile	Asn	Asn	Phe	Gly	Asp	Ser	Ile	Asn	Glu	Ser
	485								490					495		
	Glu	Gly	Ile	Pro	Leu	Lys	Arg	Arg	Arg	Val	Ser	Phe	Gly	Gly	His	Leu
	500								505					510		
30	Arg	Pro	Glu	Leu	Phe	Asp	Glu	Asn	Leu	Pro	Pro	Asn	Thr	Pro	Leu	Lys
	515								520					525		
35	Arg	Gly	Glu	Ala	Pro	Thr	Lys	Arg	Lys	Ser	Leu	Val	Met	His	Thr	Pro
	530						535					540				
	Pro	Val	Leu	Lys	Lys	Ile	Ile	Lys	Glu	Gln	Pro	Gln	Pro	Ser	Gly	Lys
	545						550					555				560
40	Gln	Glu	Ser	Gly	Ser	Glu	Ile	His	Val	Glu	Val	Lys	Ala	Gln	Ser	Leu
	565								570					575		
	Val	Ile	Ser	Pro	Pro	Ala	Pro	Ser	Pro	Arg	Lys	Thr	Pro	Val	Ala	Ser
	580								585					590		
45	Asp	Gln	Arg	Arg	Arg	Ser	Cys	Lys	Thr	Ala	Pro	Ala	Ser	Ser	Ser	Lys
	595							600					605			
	Ser	Gln	Thr	Glu	Val	Pro	Lys	Arg	Gly	Gly	Glu	Arg	Val	Ala	Thr	Cys
	610						615					620				
	Leu	Gln	Lys	Arg	Val	Ser	Ile	Ser	Arg	Ser	Gln	His	Asp	Ile	Leu	Gln
	625						630					635				640
55	Met	Ile	Cys	Ser	Lys	Arg	Arg	Ser	Gly	Ala	Ser	Glu	Ala	Asn	Leu	Ile
	645							650					655			
	Val	Ala	Lys	Ser	Trp	Ala	Asp	Val	Val	Lys	Leu	Gly	Ala	Lys	Gln	Thr
	660							665					670			
60	Gln	Thr	Lys	Val	Ile	Lys	His	Gly	Pro	Gln	Arg	Ser	Met	Asn	Lys	Arg
	675							680					685			
65	Gln	Arg	Arg	Pro	Ala	Thr	Pro	Lys	Lys	Pro	Val	Gly	Glu	Val	His	Ser
	690							695					700			

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	Gln	Phe	Ser	Thr	Gly	His	Ala	Asn	Ser	Pro	Cys	Thr	Ile	Ile	Ile	Gly
	705				710					715						720
5	Lys	Ala	His	Thr	Glu	Lys	Val	His	Val	Pro	Ala	Arg	Pro	Tyr	Arg	Val
		725				730						735				
	Leu	Asn	Asn	Phe	Ile	Ser	Asn	Gln	Lys	Met	Asp	Phe	Lys	Glu	Asp	Leu
		740					745						750			
10	Ser	Gly	Ile	Ala	Glu	Met	Phe	Lys	Thr	Pro	Val	Lys	Glu	Gln	Pro	Gln
			755			760						765				
	Leu	Thr	Ser	Thr	Cys	His	Ile	Ala	Ile	Ser	Asn	Ser	Glu	Asn	Leu	Leu
		770				775						780				
15	Gly	Lys	Gln	Phe	Gln	Gly	Thr	Asp	Ser	Gly	Glu	Glu	Pro	Leu	Leu	Pro
		785				790					795					800
20	Thr	Ser	Glu	Ser	Phe	Gly	Gly	Asn	Val	Phe	Phe	Ser	Ala	Gln	Asn	Ala
			805				810						815			
	Ala	Lys	Gln	Pro	Ser	Asp	Lys	Cys	Ser	Ala	Ser	Pro	Pro	Leu	Arg	Arg
		820					825							830		
25	Gln	Cys	Ile	Arg	Glu	Asn	Gly	Asn	Val	Ala	Lys	Thr	Pro	Arg	Asn	Thr
		835					840					845				
	Tyr	Lys	Met	Thr	Ser	Leu	Glu	Thr	Lys	Thr	Ser	Asp	Thr	Glu	Thr	Glu
		850					855					860				
30	Pro	Ser	Lys	Thr	Val	Ser	Thr	Val	Asn	Arg	Ser	Gly	Arg	Ser	Thr	Glu
		865				870				875			880			
	Phe	Arg	Asn	Ile	Gln	Lys	Leu	Pro	Val	Glu	Ser	Lys	Ser	Glu	Glu	Thr
			885				890						895			
	Asn	Thr	Glu	Ile	Val	Glu	Cys	Ile	Leu	Lys	Arg	Gly	Gln	Lys	Ala	Thr
			900					905					910			
40	Leu	Leu	Gln	Gln	Arg	Arg	Glu	Gly	Glu	Met	Lys	Glu	Ile	Glu	Arg	Pro
			915					920					925			
	Phe	Glu	Thr	Tyr	Lys	Glu	Asn	Ile	Glu	Leu	Lys	Glu	Asn	Asp	Glu	Lys
		930				935						940				
45	Met	Lys	Ala	Met	Lys	Arg	Ser	Arg	Thr	Trp	Gly	Gln	Lys	Cys	Ala	Pro
		945				950					955					960
	Met	Ser	Asp	Leu	Thr	Asp	Leu	Lys	Ser	Leu	Pro	Asp	Thr	Glu	Leu	Met
			965				970						975			
	Lys	Asp	Thr	Ala	Arg	Gly	Gln	Asn	Leu	Leu	Gln	Thr	Gln	Asp	His	Ala
			980				985						990			
55	Lys	Ala	Pro	Lys	Ser	Glu	Lys	Gly	Lys	Ile	Thr	Lys	Met	Pro	Cys	Gln
			995				1000						1005			
	Ser	Leu	Gln	Pro	Glu	Pro	Ile	Asn	Thr	Pro	Thr	His	Thr	Lys	Gln	Gln
			1010			1015						1020				
60	Leu	Lys	Ala	Ser	Leu	Gly	Lys	Val	Gly	Val	Lys	Glu	Glu	Leu	Leu	Ala
		1025				1030					1035					1040

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	Thr Pro Leu Glu Lys Arg Asp Val Gln Lys Glu Leu Ser Ala Leu Lys			
	1395	1400	1405	
5	Lys Leu Thr Gln Thr Ser Gly Glu Thr Thr His Thr Asp Lys Val Pro			
	1410	1415	1420	
	Gly Gly Glu Asp Lys Ser Ile Asn Ala Phe Arg Glu Thr Ala Lys Gln			
	1425	1430	1435	1440
10	Lys Leu Asp Pro Ala Ala Ser Val Thr Gly Ser Lys Arg His Pro Lys			
	1445	1450	1455	
	Thr Lys Glu Lys Ala Gln Pro Leu Glu Asp Leu Ala Gly Trp Lys Glu			
	1460	1465	1470	
15	Leu Phe Gln Thr Pro Val Cys Thr Asp Lys Pro Thr Thr His Glu Lys			
	1475	1480	1485	
20	Thr Thr Lys Ile Ala Cys Arg Ser Gln Pro Asp Pro Val Asp Thr Pro			
	1490	1495	1500	
	Thr Ser Ser Lys Pro Gln Ser Lys Arg Ser Leu Arg Lys Val Asp Val			
	1505	1510	1515	1520
25	Glu Glu Glu Phe Phe Ala Leu Arg Lys Arg Thr Pro Ser Ala Gly Lys			
	1525	1530	1535	
	Ala Met His Thr Pro Lys Pro Ala Val Ser Gly Glu Lys Asn Ile Tyr			
	1540	1545	1550	
30	Ala Phe Met Gly Thr Pro Val Gln Lys Leu Asp Leu Thr Glu Asn Leu			
	1555	1560	1565	
35	Thr Gly Ser Lys Arg Arg Leu Gln Thr Pro Lys Glu Lys Ala Gln Ala			
	1570	1575	1580	
	Leu Glu Asp Leu Ala Gly Phe Lys Glu Leu Phe Gln Thr Arg Gly His			
	1585	1590	1595	1600
40	Thr Glu Glu Ser Met Thr Asn Asp Lys Thr Ala Lys Val Ala Cys Lys			
	1605	1610	1615	
	Ser Ser Gln Pro Asp Leu Asp Lys Asn Pro Ala Ser Ser Lys Arg Arg			
	1620	1625	1630	
45	Leu Lys Thr Ser Leu Gly Lys Val Gly Val Lys Glu Glu Leu Leu Ala			
	1635	1640	1645	
50	Val Gly Lys Leu Thr Gln Thr Ser Gly Glu Thr Thr His Thr His Thr			
	1650	1655	1660	
	Glu Pro Thr Gly Asp Gly Lys Ser Met Lys Ala Phe Met Glu Ser Pro			
	1665	1670	1675	1680
55	Lys Gln Ile Leu Asp Ser Ala Ala Ser Leu Thr Gly Ser Lys Arg Gln			
	1685	1690	1695	
	Leu Arg Thr Pro Lys Gly Lys Ser Glu Val Pro Glu Asp Leu Ala Gly			
	1700	1705	1710	
60	Phe Ile Glu Leu Phe Gln Thr Pro Ser His Thr Lys Glu Ser Met Thr			
	1715	1720	1725	

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	Asn Glu Lys Thr Thr Lys Val Ser Tyr Arg Ala Ser Gln Pro Asp Leu
	1730 1735 1740
5	Val Asp Thr Pro Thr Ser Ser Lys Pro Gln Pro Lys Arg Ser Leu Arg
	1745 1750 1755 1760
	Lys Ala Asp Thr Glu Glu Phe Leu Ala Phe Arg Lys Gln Thr Pro
	1765 1770 1775
10	Ser Ala Gly Lys Ala Met His Thr Pro Lys Pro Ala Val Gly Glu Glu
	1780 1785 1790
	Lys Asp Ile Asn Thr Phe Leu Gly Thr Pro Val Gln Lys Leu Asp Gln
	1795 1800 1805
15	Pro Gly Asn Leu Pro Gly Ser Asn Arg Arg Leu Gln Thr Arg Lys Glu
	1810 1815 1820
20	Lys Ala Gln Ala Leu Glu Glu Leu Thr Gly Phe Arg Glu Leu Phe Gln
	1825 1830 1835 1840
	Thr Pro Cys Thr Asp Asn Pro Thr Ala Asp Glu Lys Thr Thr Lys Lys
	1845 1850 1855
25	Ile Leu Cys Lys Ser Pro Gln Ser Asp Pro Ala Asp Thr Pro Thr Asn
	1860 1865 1870
	Thr Lys Gln Arg Pro Lys Arg Ser Leu Lys Lys Ala Asp Val Glu Glu
	1875 1880 1885
30	Glu Phe Leu Ala Phe Arg Lys Leu Thr Pro Ser Ala Gly Lys Ala Met
	1890 1895 1900
	His Thr Pro Lys Ala Ala Val Gly Glu Glu Lys Asp Ile Asn Thr Phe
35	1905 1910 1915 1920
	Val Gly Thr Pro Val Glu Lys Leu Asp Leu Leu Gly Asn Leu Pro Gly
	1925 1930 1935
40	Ser Lys Arg Arg Pro Gln Thr Pro Lys Glu Lys Ala Lys Ala Leu Glu
	1940 1945 1950
	Asp Leu Ala Gly Phe Lys Glu Leu Phe Gln Thr Pro Gly His Thr Glu
	1955 1960 1965
45	Glü Ser Met Thr Asp Asp Lys Ile Thr Glu Val Ser Cys Lys Ser Pro
	1970 1975 1980
	Gln Pro Asp Pro Val Lys Thr Pro Thr Ser Ser Lys Gln Arg Leu Lys
50	1985 1990 1995 2000
	Ile Ser Leu Gly Lys Val Gly Val Lys Glu Glu Val Leu Pro Val Gly
	2005 2010 2015
55	Lys Leu Thr Gln Thr Ser Gly Lys Thr Thr Gln Thr His Arg Glu Thr
	2020 2025 2030
	Ala Gly Asp Gly Lys Ser Ile Lys Ala Phe Lys Glu Ser Ala Lys Gln
	2035 2040 2045
60	Met Leu Asp Pro Ala Asn Tyr Gly Thr Gly Met Glu Arg Trp Pro Arg
	2050 2055 2060
65	Thr Pro Lys Glu Glu Ala Gln Ser Leu Glu Asp Leu Ala Gly Phe Lys
	2065 2070 2075 2080

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Glu Leu Phe Gln Thr Pro Asp His Thr Glu Glu Ser Thr Thr Asp Asp
 2085 2090 2095
 Lys Thr Thr Lys Ile Ala Cys Lys Ser Pro Pro Pro Glu Ser Met Asp
 5 2100 2105 2110
 Thr Pro Thr Ser Thr Arg Arg Arg Pro Lys Thr Pro Leu Gly Lys Arg
 2115 2120 2125
 10 Asp Ile Val Glu Glu Leu Ser Ala Leu Lys Gln Leu Thr Gln Thr Thr
 2130 2135 2140
 His Thr Asp Lys Val Pro Gly Asp Glu Asp Lys Gly Ile Asn Val Phe
 2145 2150 2155 2160
 15 Arg Glu Thr Ala Lys Gln Lys Leu Asp Pro Ala Ala Ser Val Thr Gly
 2165 2170 2175
 Ser Lys Arg Gln Pro Arg Thr Pro Lys Gly Lys Ala Gln Pro Leu Glu
 20 2180 2185 2190
 Asp Leu Ala Gly Leu Lys Glu Leu Phe Gln Thr Pro Val Cys Thr Asp
 2195 2200 2205
 25 Lys Pro Thr Thr His Glu Lys Thr Thr Lys Ile Ala Cys Arg Ser Pro
 2210 2215 2220
 Gln Pro Asp Pro Val Gly Thr Pro Thr Ile Phe Lys Pro Gln Ser Lys
 2225 2230 2235 2240
 30 Arg Ser Leu Arg Lys Ala Asp Val Glu Glu Glu Ser Leu Ala Leu Arg
 2245 2250 2255
 Lys Arg Thr Pro Ser Val Gly Lys Ala Met Asp Thr Pro Lys Pro Ala
 35 2260 2265 2270
 Gly Gly Asp Glu Lys Asp Met Lys Ala Phe Met Gly Thr Pro Val Gln
 2275 2280 2285
 40 Lys Leu Asp Leu Pro Gly Asn Leu Pro Gly Ser Lys Arg Trp Pro Gln
 2290 2295 2300
 Thr Pro Lys Glu Lys Ala Gln Ala Leu Glu Asp Leu Ala Gly Phe Lys
 2305 2310 2315 2320
 45 Glu Leu Phe Gln Thr Pro Gly Thr Asp Lys Pro Thr Thr Asp Glu Lys
 2325 2330 2335
 Thr Thr Lys Ile Ala Cys Lys Ser Pro Gln Pro Asp Pro Val Asp Thr
 50 2340 2345 2350
 Pro Ala Ser Thr Lys Gln Arg Pro Lys Arg Asn Leu Arg Lys Ala Asp
 2355 2360 2365
 55 Val Glu Glu Glu Phe Leu Ala Leu Arg Lys Arg Thr Pro Ser Ala Gly
 2370 2375 2380
 Lys Ala Met Asp Thr Pro Lys Pro Ala Val Ser Asp Glu Lys Asn Ile
 2385 2390 2395 2400
 60 Asn Thr Phe Val Glu Thr Pro Val Gln Lys Leu Asp Leu Leu Gly Asn
 2405 2410 2415

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	Leu Pro Gly Ser Lys Arg Gln Pro Gln Thr Pro Lys Glu Lys Ala Glu			
	2420	2425	2430	
5	Ala Leu Glu Asp Leu Val Gly Phe Lys Glu Leu Phe Gln Thr Pro Gly			
	2435	2440	2445	
	His Thr Glu Glu Ser Met Thr Asp Asp Lys Ile Thr Glu Val Ser Cys			
	2450	2455	2460	
10	Lys Ser Pro Gln Pro Glu Ser Phe Lys Thr Ser Arg Ser Ser Lys Gln			
	2465	2470	2475	2480
	Arg Leu Lys Ile Pro Leu Val Lys Val Asp Met Lys Glu Glu Pro Leu			
	2485	2490	2495	
15	Ala Val Ser Lys Leu Thr Arg Thr Ser Gly Glu Thr Thr Gln Thr His			
	2500	2505	2510	
20	Thr Glu Pro Thr Gly Asp Ser Lys Ser Ile Lys Ala Phe Lys Glu Ser			
	2515	2520	2525	
	Pro Lys Gln Ile Leu Asp Pro Ala Ala Ser Val Thr Gly Ser Arg Arg			
	2530	2535	2540	
25	Gln Leu Arg Thr Arg Lys Glu Lys Ala Arg Ala Leu Glu Asp Leu Val			
	2545	2550	2555	2560
	Asp Phe Lys Glu Leu Phe Ser Ala Pro Gly His Thr Glu Glu Ser Met			
	2565	2570	2575	
30	Thr Ile Asp Lys Asn Thr Lys Ile Pro Cys Lys Ser Pro Pro Pro Glu			
	2580	2585	2590	
35	Leu Thr Asp Thr Ala Thr Ser Thr Lys Arg Cys Pro Lys Thr Arg Pro			
	2595	2600	2605	
	Arg Lys Glu Val Lys Glu Glu Leu Ser Ala Val Glu Arg Leu Thr Gln			
	2610	2615	2620	
40	Thr Ser Gly Gln Ser Thr His Thr His Lys Glu Pro Ala Ser Gly Asp			
	2625	2630	2635	2640
	Glu Gly Ile Lys Val Leu Lys Gln Arg Ala Lys Lys Pro Asn Pro			
	2645	2650	2655	
45	Val Glu Glu Glu Pro Ser Arg Arg Arg Pro Arg Ala Pro Lys Glu Lys			
	2660	2665	2670	
50	Ala Gln Pro Leu Glu Asp Leu Ala Gly Phe Thr Glu Leu Ser Glu Thr			
	2675	2680	2685	
	Ser Gly His Thr Gln Glu Ser Leu Thr Ala Gly Lys Ala Thr Lys Ile			
	2690	2695	2700	
55	Pro Cys Glu Ser Pro Pro Leu Glu Val Val Asp Thr Thr Ala Ser Thr			
	2705	2710	2715	2720
	Lys Arg His Leu Arg Thr Arg Val Gln Lys Val Gln Val Lys Glu Glu			
	2725	2730	2735	
60	Pro Ser Ala Val Lys Phe Thr Gln Thr Ser Gly Glu Thr Thr Asp Ala			
	2740	2745	2750	
65	Asp Lys Glu Pro Ala Gly Glu Asp Lys Gly Ile Lys Ala Leu Lys Glu			
	2755	2760	2765	

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Ser Ala Lys Gln Thr Pro Ala Pro Ala Ala Ser Val Thr Gly Ser Arg
 2770 2775 2780
 Arg Arg Pro Arg Ala Pro Arg Glu Ser Ala Gln Ala Ile Glu Asp Leu
 5 2785 2790 2795 2800
 Ala Gly Phe Lys Asp Pro Ala Ala Gly His Thr Glu Glu Ser Met Thr
 2805 2810 2815
 10 Asp Asp Lys Thr Thr Lys Ile Pro Cys Lys Ser Ser Pro Glu Leu Glu
 2820 2825 2830
 Asp Thr Ala Thr Ser Ser Lys Arg Arg Pro Arg Thr Arg Ala Gln Lys
 2835 2840 2845
 15 Val Glu Val Lys Glu Glu Leu Leu Ala Val Gly Lys Leu Thr Gln Thr
 2850 2855 2860
 Ser Gly Glu Thr Thr His Thr Asp Lys Glu Pro Val Gly Glu Gly Lys
 20 2865 2870 2875 2880
 Gly Thr Lys Ala Phe Lys Gln Pro Ala Lys Arg Asn Val Asp Ala Glu
 2885 2890 2895
 25 Asp Val Ile Gly Ser Arg Arg Gln Pro Arg Ala Pro Lys Glu Lys Ala
 2900 2905 2910
 Gln Pro Leu Glu Asp Leu Ala Ser Phe Gln Glu Leu Ser Gln Thr Pro
 30 2915 2920 2925
 Gly His Thr Glu Glu Leu Ala Asn Gly Ala Ala Asp Ser Phe Thr Ser
 2930 2935 2940
 Ala Pro Lys Gln Thr Pro Asp Ser Gly Lys Pro Leu Lys Ile Ser Arg
 35 2945 2950 2955 2960
 Arg Val Leu Arg Ala Pro Lys Val Glu Pro Val Gly Asp Val Val Ser
 2965 2970 2975
 40 Thr Arg Asp Pro Val Lys Ser Gln Ser Lys Ser Asn Thr Ser Leu Pro
 2980 2985 2990
 Pro Leu Pro Phe Lys Arg Gly Gly Lys Asp Gly Ser Val Thr Gly
 2995 3000 3005
 45 Thr Lys Arg Leu Arg Cys Met Pro Ala Pro Glu Glu Ile Val Glu Glu
 3010 3015 3020
 Leu Pro Ala Ser Lys Lys Gln Arg Val Ala Pro Arg Ala Arg Gly Lys
 50 3025 3030 3035 3040
 Ser Ser Glu Pro Val Val Ile Met Lys Arg Ser Leu Arg Thr Ser Ala
 3045 3050 3055
 55 Lys Arg Ile Glu Pro Ala Glu Glu Leu Asn Ser Asn Asp Met Lys Thr
 3060 3065 3070
 Asn Lys Glu Glu His Lys Leu Gln Asp Ser Val Pro Glu Asn Lys Gly
 60 3075 3080 3085
 Ile Ser Leu Arg Ser Arg Arg Gln Asp Lys Thr Glu Ala Glu Gln Gln
 3090 3095 3100

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Ile Thr Glu Val Phe Val Leu Ala Glu Arg Ile Glu Ile Asn Arg Asn
3105 3110 3115 3120

5 Glu Lys Lys Pro Met Lys Thr Ser Pro Glu Met Asp Ile Gln Asn Pro
3125 3130 3135

Asp Asp Gly Ala Arg Lys Pro Ile Pro Arg Asp Lys Val Thr Glu Asn
3140 3145 3150

10 Lys Arg Cys Leu Arg Ser Ala Arg Gln Asn Glu Ser Ser Gln Pro Lys
3155 3160 3165

Val Ala Glu Glu Ser Gly Gly Gln Lys Ser Ala Lys Val Leu Met Gln
3170 3175 3180

15 Asn Gln Lys Gly Lys Gly Glu Ala Gly Asn Ser Asp Ser Met Cys Leu
3185 3190 3195 3200

20 Arg Ser Arg Lys Thr Lys Ser Gln Pro Ala Ala Ser Thr Leu Glu Ser
3205 3210 3215

Lys Ser Val Gln Arg Val Thr Arg Ser Val Lys Arg Cys Ala Glu Asn
3220 3225 3230

25 Pro Lys Lys Ala Glu Asp Asn Val Cys Val Lys Lys Ile Thr Thr Arg
3235 3240 3245

Ser His Arg Asp Ser Glu Asp Ile
3250 3255

30 (2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS

- (A) LENGTH: 23 base pairs
- (B) TYPE: Nucleotid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) description: /desc = "synthetic oligonucleotide"

45 (xi) SEQUENCE DISCRIPTION: SEQ ID NO: 3:

ACCAAGGCGTC TCGTGGGCCA CAT

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